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PATENT

Docket No.: 201040/1020

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) : Alam et al.

Serial No. : 09/455,978

Cnfrm. No. : 5811

Filed : December 6, 1999

For : HEME PROTEINS HEMAT-*HS* AND  
HEMAT-*BS* AND THEIR USE IN  
MEDICINE AND MICROSENSORS

Examiner:  
H. Schnizer

Art Unit:  
1653

Commissioner for Patents  
Washington, D.C. 20231  
Box: SEQUENCE

BEST AVAILABLE COPY

Dear Sir:

Transmitted herewith in the above-identified application are:

- ☒ Request for One-Month Extension of Time.
- ☒ Statement in Accordance with 37 C.F.R. § 1.821(g), Sequence Listing (38 pages), and computer readable 3.5" Diskette.
- ☒ Copy of Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures and Raw Sequence Listing Error Report; and
- ☒ A self-addressed postcard for acknowledging receipt.

- ☒ The Commissioner is hereby authorized to charge any additional fees or credit any overpayment to Deposit Account No. 14-1138.

A duplicate copy of this sheet is enclosed.

Date: October 23, 2001

Edwin V. Merkel  
Registration No. 40,087

Nixon Peabody LLP  
Clinton Square, P.O. Box 31051  
Rochester, New York 14603-1051  
Telephone: (716) 263-1128  
Facsimile: (716) 263-1600

RS29962.1

Certificate of Mailing - 37 CFR 1.8(a)	
I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231, on the date below.	
Date 10/23/01	 Jo Ann Whalen

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g).

For questions regarding compliance to these requirements, please contact:

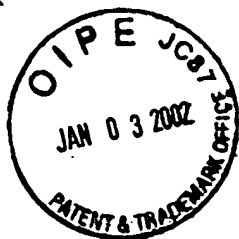
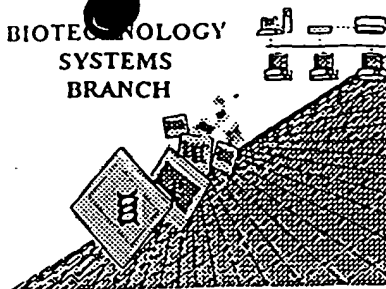
- For Rules Interpretation, call (703) 308-4216 or (703) 308-2923
- For CRF Submission Help, call (703) 308-4212
- For PatentIn software Program Support:
  - HELP DESK: (703) 739-8559, ext 508, M-F, 8 AM to 5 PM EST except holidays
  - Email: [PATIN21HELP@uspto.gov](mailto:PATIN21HELP@uspto.gov)
  - To purchase PatentIn software: (703) 306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

*H. Schnitzer*

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/455,978

Source: OIPE

Date Processed by STIC: 7/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

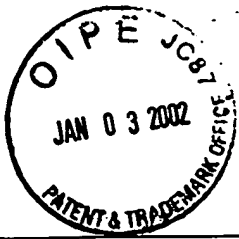
### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/455,978

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi)      SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>    Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.



Re-run

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001

TIME: 13:15:00

Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

Does Not Comply  
Corrected Diskette Needed

see page 5

3 <110> APPLICANT: Alam, Maqsudul  
4 Larsen, Randy  
6 <120> TITLE OF INVENTION: HEME PROTEINS HEMAT-HS AND HEMAT-BS AND THEIR USE IN  
7 MEDICINE AND MICROSENSORS  
9 <130> FILE REFERENCE: 201040/1020  
11 <140> CURRENT APPLICATION NUMBER: 09/455,978  
12 <141> CURRENT FILING DATE: 1999-12-06  
14 <160> NUMBER OF SEQ ID NOS: 86  
16 <170> SOFTWARE: PatentIn Ver. 2.1  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 1470  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Halobacterium salinarum  
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25 gcaactcgcg accgcatcgg cctcgacgag gcggagatcg cgtggcggct gtcgttcacc 120  
26 gggatcgacg acgacacgat ggccgcgctc gccgccgaac agccgctgtt cgaagccacc 180  
27 gcggacgcgc tgggtgaccga cttctacgac cacttgaggt cctacgagcg cacacaggac 240  
28 ctcttcgega actccacgaa gaccgtcgag caactcaaag agacgcaggc cgagtacttg 300  
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34 atcgacagcc gccaggagtt ggcgaaacgc gtcgccacgc acgtggaagc accgctgtcc 660  
35 tcgctggagg cgacctcgca ggacgtcgcc gagcgacgg acacgatgcg ggcccgacc 720  
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38 ctggcccgac agggcgaggc ggccgcggac gacgcgtcgc ccacgatgac cgacatcgac 900  
39 gaggcgaccg acggcgctac cgcgggcgtc gaacagctcg gcgagcgcgc cgccgacgtc 960  
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41 gcgtccatcg aggcgcgccg cgcgggggag gcgggcgagg ggtttgcggt cgtcgccgac 1080  
42 gaggtcaagg ccctcgccga ggagtccgcg gagcagtcca cgcgcgtcga ggagctcgtc 1140  
43 gagcagatgc aggcggagac cgaggagacg gtcgaccagt tggacgaggt caaccagcgc 1200  
44 atcggcgagg gcgtcgagcg cgtcgaggag gcgatggaga ccctccagga gatcaccgac 1260  
45 gccgtcgagg acgcgcgaag cgggatgcag gaggtgtcga cggcgaccga cgaacaggcg 1320  
46 gtgagcaccg aggaggtcgc cgagatggtc gacggtgtcg acgaccgcgc gggcgagatc 1380  
47 gcggccgccc tcgatgacat cgcgcgacgc accgatcagc aggtccggac cgtcgaggag 1440  
48 gtccgcgaga cggtcggcaa gctcagctag 1470  
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52 <211> LENGTH: 489  
53 <212> TYPE: PRT  
54 <213> ORGANISM: Halobacterium salinarum  
56 <400> SEQUENCE: 2  
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58 1 5 10 15  
60 Ile Asp Gly His Ala Leu Ala Asp Arg Ile Gly Leu Asp Glu Ala Glu

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001

TIME: 13:15:00

Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

```

61          20          25          30
63 Ile Ala Trp Arg Leu Ser Phe Thr Gly Ile Asp Asp Asp Thr Met Ala
64          35          40          45
66 Ala Leu Ala Ala Glu Gln Pro Leu Phe Glu Ala Thr Ala Asp Ala Leu
67          50          55          60
69 Val Thr Asp Phe Tyr Asp His Leu Glu Ser Tyr Glu Arg Thr Gln Asp
70          65          70          75          80
72 Leu Phe Ala Asn Ser Thr Lys Thr Val Glu Gln Leu Lys Glu Thr Gln
73          85          90          95
75 Ala Glu Tyr Leu Leu Gly Leu Gly Arg Gly Glu Tyr Asp Thr Glu Tyr
76          100          105          110
78 Ala Ala Gln Arg Ala Arg Ile Gly Lys Ile His Asp Val Leu Gly Leu
79          115          120          125
81 Gly Pro Asp Val Tyr Leu Gly Ala Tyr Thr Arg Tyr Thr Gly Leu
82          130          135          140
84 Leu Asp Ala Leu Ala Asp Asp Val Val Ala Asp Arg Gly Glu Glu Ala
85          145          150          155          160
87 Ala Ala Ala Val Asp Glu Leu Val Ala Arg Phe Leu Pro Met Leu Lys
88          165          170          175
90 Leu Leu Thr Phe Asp Gln Gln Ile Ala Met Asp Thr Tyr Ile Asp Ser
91          180          185          190
93 Tyr Ala Gln Arg Leu His Asp Glu Ile Asp Ser Arg Gln Glu Leu Ala
94          195          200          205
96 Asn Ala Val Ala Thr His Val Glu Ala Pro Leu Ser Ser Leu Glu Ala
97          210          215          220
99 Thr Ser Gln Asp Val Ala Glu Arg Thr Asp Thr Met Arg Ala Arg Thr
100          225          230          235          240
102 Asp Asp Gln Val Asp Arg Met Ala Asp Val Ser Arg Glu Ile Ser Ser
103          245          250          255
105 Val Ser Ala Ser Val Glu Glu Val Ala Ser Thr Ala Asp Asp Val Arg
106          260          265          270
108 Arg Thr Ser Glu Asp Ala Glu Ala Leu Ala Gln Gln Gly Glu Ala Ala
109          275          280          285
111 Ala Asp Asp Ala Leu Ala Thr Met Thr Asp Ile Asp Glu Ala Thr Asp
112          290          295          300
114 Gly Val Thr Ala Gly Val Glu Gln Leu Gly Glu Arg Ala Ala Asp Val
115          305          310          315          320
117 Glu Ser Val Thr Gly Val Ile Asp Asp Ile Ala Glu Gln Thr Asn Met
118          325          330          335
120 Leu Ala Leu Asn Ala Ser Ile Glu Ala Ala Arg Ala Gly Glu Ala Gly
121          340          345          350
123 Glu Gly Phe Ala Val Val Ala Asp Glu Val Lys Ala Leu Ala Glu Glu
124          355          360          365
126 Ser Arg Glu Gln Ser Thr Arg Val Glu Glu Leu Val Glu Gln Met Gln
127          370          375          380
129 Ala Glu Thr Glu Glu Thr Val Asp Gln Leu Asp Glu Val Asn Gln Arg
130          385          390          395          400
132 Ile Gly Glu Gly Val Glu Arg Val Glu Glu Ala Met Glu Thr Leu Gln
133          405          410          415

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001

TIME: 13:15:00

Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

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135 Glu Ile Thr Asp Ala Val Glu Asp Ala Ala Ser Gly Met Gln Glu Val
136          420          425          430
138 Ser Thr Ala Thr Asp Glu Gln Ala Val Ser Thr Glu Glu Val Ala Glu
139          435          440          445
141 Met Val Asp Gly Val Asp Asp Arg Ala Gly Glu Ile Ala Ala Ala Leu
142          450          455          460
144 Asp Asp Ile Ala Asp Ala Thr Asp Gln Gln Val Arg Thr Val Glu Glu
145 465          470          475          480
147 Val Arg Glu Thr Val Gly Lys Leu Ser
148          485
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152 <211> LENGTH: 1390
153 <212> TYPE: DNA
154 <213> ORGANISM: Bacillus subtilis
156 <400> SEQUENCE: 3
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158 caaaaaaacc gcattcagct cacaacacaa catgcagatg tcaaaaaaca gctcaaaatg 120
159 gtcagggttg gagatgctga gctttatgtg ttagagcagc ttcagccact cattcaagaa 180
160 aatatcgtaa atatcgctga tgcgttttat aaaaaccttg accatgaaag ctcatgatg 240
161 gatatcatta atgatcacag ctcatgtgac cgcttaaaac aaacgttaaa acggcatatt 300
162 caggaaatgt ttgcaggcgt tatcgatgat gaatttattg aaaagcgtaa ccgaatcgcc 360
163 tccatccatt taagaatcgg ccttttgcca aaatggtata tgggtgctgt tcaagagctc 420
164 cttttgtcaa tgattgacat ttatgaagcg tccattacaa atcagcaaga actgctaaaa 480
165 gccattaaag caacaacaaa aatcttgaac ttagaacagc agcttgtcct tgaagcgttt 540
166 caaagcgagt acaaccagac ccgtgatgaa caagaagaaa agaaaaacct tcttcatcag 600
167 aaaattcaag aaacctctgg atcgattgcc attctgtttt cagaaacaag cagatcagtt 660
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170 cagatgaaca aaattgacac aagccttgtc caaatcgaaa aagaaatggt caagctggat 840
171 gaaatcgcg agcaaattga aaaaatcttc ggcacgtea caggcatagc tgaacaaaa 900
172 aaccttctct cgtcfaatgc atctattgaa tccgcccgcg ccggagaaca cggcaaaggc 960
173 tttgctgtcg tggcaaatga agtgcggaag ctttctgagg atacgaaaaa aaccgtctct 1020
174 actgtttctg agcttgtgaa caatacgaat acacaaatca acattgtatc caagcatatc 1080
175 aaagacgtga atgagctagt cagcgaaagt aaagaaaaaa tgacgcaaat taaccgctta 1140
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177 gatctgcaag cctttcttgg agggcttcag gaagtcagcc gcgcccgttc ccatgtggcc 1260
178 gcttccgttg attcgttgt catcctgaca gaagaataac catcaaaaac cggctctgcca 1320
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192 Ser Asn Gly Gln Gln Lys Asn Arg Ile Gln Leu Thr Asn Lys His Ala
193 20 25 30
195 Asp Val Lys Lys Gln Leu Lys Met Val Arg Leu Gly Asp Ala Glu Leu

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001

TIME: 13:15:00

Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

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196          35          40          45
198 Tyr Val Leu Glu Gln Leu Gln Pro Leu Ile Gln Glu Asn Ile Val Asn
199          50          55          60
201 Ile Val Asp Ala Phe Tyr Lys Asn Leu Asp His Glu Ser Ser Leu Met
202 65          70          75          80
204 Asp Ile Ile Asn Asp His Ser Ser Val Asp Arg Leu Lys Gln Thr Leu
205          85          90          95
207 Lys Arg His Ile Gln Glu Met Phe Ala Gly Val Ile Asp Asp Glu Phe
208          100          105          110
210 Ile Glu Lys Arg Asn Arg Ile Ala Ser Ile His Leu Arg Ile Gly Leu
211          115          120          125
213 Leu Pro Lys Trp Tyr Met Gly Ala Phe Gln Glu Leu Leu Leu Ser Met
214          130          135          140
216 Ile Asp Ile Tyr Glu Ala Ser Ile Thr Asn Gln Gln Glu Leu Leu Lys
217 145          150          155          160
219 Ala Ile Lys Ala Thr Thr Lys Ile Leu Asn Leu Glu Gln Gln Leu Val
220          165          170          175
222 Leu Glu Ala Phe Gln Ser Glu Tyr Asn Gln Thr Arg Asp Glu Gln Glu
223          180          185          190
225 Glu Lys Lys Asn Leu Leu His Gln Lys Ile Gln Glu Thr Ser Gly Ser
226          195          200          205
228 Ile Ala Asn Leu Phe Ser Glu Thr Ser Arg Ser Val Gln Glu Leu Val
229          210          215          220
231 Asp Lys Ser Glu Gly Ile Ser Gln Ala Ser Lys Ala Gly Thr Val Thr
232 225          230          235          240
234 Ser Ser Thr Val Glu Glu Lys Ser Ile Gly Gly Lys Lys Glu Leu Glu
235          245          250          255
237 Val Gln Gln Lys Gln Met Asn Lys Ile Asp Thr Ser Leu Val Gln Ile
238          260          265          270
240 Glu Lys Glu Met Val Lys Leu Asp Glu Ile Ala Gln Gln Ile Glu Lys
241          275          280          285
243 Ile Phe Gly Ile Val Thr Gly Ile Ala Glu Gln Thr Asn Leu Leu Ser
244          290          295          300
246 Leu Asn Ala Ser Ile Glu Ser Ala Arg Ala Gly Glu His Gly Lys Gly
247 305          310          315          320
249 Phe Ala Val Val Ala Asn Glu Val Arg Lys Leu Ser Glu Asp Thr Lys
250          325          330          335
252 Lys Thr Val Ser Thr Val Ser Glu Leu Val Asn Asn Thr Asn Thr Gln
253          340          345          350
255 Ile Asn Ile Val Ser Lys His Ile Lys Asp Val Asn Glu Leu Val Ser
256          355          360          365
258 Glu Ser Lys Glu Lys Met Thr Gln Ile Asn Arg Leu Phe Asp Glu Ile
259          370          375          380
261 Val His Ser Met Lys Ile Ser Lys Glu Gln Ser Gly Lys Ile Asp Val
262 385          390          395          400
264 Asp Leu Gln Ala Phe Leu Gly Gly Leu Gln Glu Val Ser Arg Ala Val
265          405          410          415
267 Ser His Val Ala Ala Ser Val Asp Ser Leu Val Ile Leu Thr Glu Glu
268          420          425          430

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001  
TIME: 13:15:00

Input Set : A:\H1020011.app  
Output Set: N:\CRF3\07062001\I455978.raw

274 <210> SEQ ID NO: 5  
275 <211> LENGTH: 57  
276 <212> TYPE: PRT  
277 <213> ORGANISM: Artificial Sequence  
279 <220> FEATURE:  
280 <223> OTHER INFORMATION: Description of Artificial Sequence: Template  
281 sequence  
283 <220> FEATURE:  
284 <221> NAME/KEY: UNSURE  
285 <222> LOCATION: (4)  
286 <223> OTHER INFORMATION: X at any position in this sequence is unknown.  
288 <400> SEQUENCE: 5

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290 1 5 10 15  
v--> 292 Gly Gln Asp Val Leu Val Val Leu Ile Lys Xaa Asn Pro Glu Ile Gln  
293 20 25 30  
v--> 295 Glu Lys Phe Phe Phe Lys His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
296 35 40 45  
v--> 298 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
299 50 55

302 <210> SEQ ID NO: 6  
303 <211> LENGTH: 55  
304 <212> TYPE: PRT  
305 <213> ORGANISM: Erwinia chrysanthemi  
307 <400> SEQUENCE: 6  
308 Ile Lys Ser Thr Ile Pro Leu Leu Ala Glu Thr Gly Pro Ala Leu Thr  
309 1 5 10 15  
311 Ala His Phe Tyr Gln Arg Met Phe His His Asn Pro Glu Leu Lys Asp  
312 20 25 30  
314 Ile Phe Asn Met Ser Asn Gln Arg Asn Gly Asp Gln Arg Glu Ala Leu  
315 35 40 45  
317 Phe Asn Ala Ile Cys Ala Tyr  
318 50 55

321 <210> SEQ ID NO: 7  
322 <211> LENGTH: 56  
323 <212> TYPE: PRT  
324 <213> ORGANISM: Vitreoscilla stercoraria  
326 <400> SEQUENCE: 7  
327 Ile Ile Lys Ala Thr Val Pro Val Leu Lys Glu His Gly Val Thr Ile  
328 1 5 10 15  
330 Thr Thr Thr Phe Tyr Lys Asn Leu Phe Ala Lys His Pro Glu Val Arg  
331 20 25 30  
333 Pro Leu Phe Asp Met Gly Arg Gln Glu Ser Leu Glu Gln Pro Lys Ala  
334 35 40 45  
336 Leu Ala Met Thr Val Leu Ala Ala  
337 50 55

340 <210> SEQ ID NO: 8  
341 <211> LENGTH: 55  
342 <212> TYPE: PRT

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

<222> must contain location of all Xaa's.  
If Xaa's are all the same use of a range  
to describe the location is fine. See item # 5  
on Error  
Summary  
Sheet

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001

TIME: 13:15:01

Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50  
L:1700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82  
L:1703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82  
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83  
L:1744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84  
L:1763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85  
L:1785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86